

0300

#5



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RAW SEQUENCE LISTING

DATE: 01/30/2002

PATENT APPLICATION: US/09/945,173

TIME: 16:21:02

Input Set : D:\38155-20035.txt

Output Set: N:\CRF3\01302002\I945173.raw

p.5

ENTERED

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4 <110> APPLICANT: Millennium Pharmaceuticals, Inc.
5   Meyers, Rachel
7 <120> TITLE OF INVENTION: 47324, A NOVEL HUMAN G-PROTEIN AND USES
8   THEREFOR
10 <130> FILE REFERENCE: 38155-20035.00
12 <140> CURRENT APPLICATION NUMBER: US 09/945,173
13 <141> CURRENT FILING DATE: 2001-08-31
15 <150> PRIOR APPLICATION NUMBER: US 60/229,293
16 <151> PRIOR FILING DATE: 2000-09-01
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 1694
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (19)...(729)
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33           Met Ala Ser Leu Asp Arg Val Lys Val Leu Val
34           1           5           10
36 ttg gga gac tca ggt gtt ggg aaa tct tcg tta gtc cat ctc cta tgc      99
37 Leu Gly Asp Ser Gly Val Gly Lys Ser Ser Leu Val His Leu Leu Cys
38           15           20           25
40 caa aat caa gtg ctg gga aat cca tca tgg act gtg ggc tgc tca gtg      147
41 Gln Asn Gln Val Leu Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val
42           30           35           40
44 gat gtc aga gtt cat gat tac aaa gaa gga acc cca gaa gag aag acc      195
45 Asp Val Arg Val His Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr
46           45           50           55
48 tac tac ata gaa tta tgg gat gtt gga ggc tct gtg ggc agt gcc agc      243
49 Tyr Tyr Ile Glu Leu Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser
50           60           65           70           75
52 agc gtg aaa agc aca aga gca gta ttc tac aac tcc gta aat ggt att      291
53 Ser Val Lys Ser Thr Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile
54           80           85           90
56 att ttc gta cac gac tta aca aat aag aag tcc tcc caa aac ttg cgt      339
57 Ile Phe Val His Asp Leu Thr Asn Lys Lys Ser Ser Gln Asn Leu Arg
58           95           100           105
60 cgt tgg tca ttg gaa gct ctc aac agg gat ttg gtg cca act gga gtc      387
61 Arg Trp Ser Leu Glu Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val
62           110           115           120

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64 ttg gtg aca aat ggg gat tat gat caa gaa cag ttt gct gat aac caa      435
65 Leu Val Thr Asn Gly Asp Tyr Asp Gln Glu Gln Phe Ala Asp Asn Gln
66      125      130      135
68 ata cca ctg ttg gta ata ggg act aaa ctg gac cag att cat gaa aca      483
69 Ile Pro Leu Leu Val Ile Gly Thr Lys Leu Asp Gln Ile His Glu Thr
70 140      145      150      155
72 aag cgc cat gaa gtt tta act agg act gct ttc ctg gct gag gat ttc      531
73 Lys Arg His Glu Val Leu Thr Arg Thr Ala Phe Leu Ala Glu Asp Phe
74      160      165      170
76 aat cca gaa gaa att aat ttg gac tgc aca aat cca cgg tac tta gct      579
77 Asn Pro Glu Glu Ile Asn Leu Asp Cys Thr Asn Pro Arg Tyr Leu Ala
78      175      180      185
80 gca ggt tct tcc aat gct gtc aag ctc agt agg ttt ttt gat aag gtc      627
81 Ala Gly Ser Ser Asn Ala Val Lys Leu Ser Arg Phe Phe Asp Lys Val
82      190      195      200
84 ata gag aag aga tac ttt tta aga gaa ggt aat cag att cca ggc ttt      675
85 Ile Glu Lys Arg Tyr Phe Leu Arg Glu Gly Asn Gln Ile Pro Gly Phe
86      205      210      215
88 cct gat cgg aaa aga ttt ggg gca gga aca tta aag agc ctt cat tat      723
89 Pro Asp Arg Lys Arg Phe Gly Ala Gly Thr Leu Lys Ser Leu His Tyr
90 220      225      230      235
92 gac tga attacactca tcctttggaa gaggtagcaa gcaaggcag tttttcacag      779
93 Asp *
96 ctcatcttgc tgtgttcaat tattaccatc acagcctttt aacaaaatca tcttaaaatg      839
97 ctacccttca gccttaccct ttaatggaaa aatgaaagga agtgacaata cgggaggtcc      899
98 aaactttgtc cctgttctct gtgttcctta cctttctgtc cctgtgtata gattatgtaa      959
99 aagccttgtg taaatatgag atgttgtcaa aatgatgcag taaatgagca atgacagtgt      1019
100 actgcagaga aaatttactc ttgcctagaa ctggagggtt tttatgggtc tgtaattttc      1079
101 ccacactcat tgcgtgaaagc ttaattaagt acttcaaaaa cgtatctcca ttgttttacc      1139
102 ttcttgaggg gaacgggtctt gtttaaccagc cctgagttgt ctaccccaaa caatctctgt      1199
103 cattttcaaa gatgcaaaat ggtgttatit aattgtctcc accattgtca cacacaggaa      1259
104 tgctaataa tagcaacctt tgtctccctc ttctctcctt tgcaaatggc tcagtactg      1319
105 gaagaggcgg actaatagcc agagttaa ataaatacaa attaataata catagagaac      1379
106 agcaatacca gaaaaaaga attctggtaa aatgatgtga aaaattgaca gctccctcac      1439
107 tcttaagggt gctgctatat acagtctagg ttttctgttt ggaaatagg agggtaaaat      1499
108 ctaagacctg cacaagggca gtgagagaca ttacagcct cctctctatt tgttttttta      1559
109 aggaaaagtc aactcctgaa atgtccctta gctataatca gaaaactaag aatattattc      1619
110 tgtgtcaaca atgtatttat ggagagaagt aaaaataagt tccacagcaa cacaaaaaca      1679
111 tgaattattg aacta
112
113 <210> SEQ ID NO: 2
114 <211> LENGTH: 236
115 <212> TYPE: PRT
116 <213> ORGANISM: Homo sapiens
117
118 <400> SEQUENCE: 2
119 Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly Asp Ser Gly
120 1      5      10      15
121 Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn Gln Val Leu
122      20      25      30
123 Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val Arg Val His

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```

124          35          40          45
125 Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr Ile Glu Leu
126          50          55          60
127 Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val Lys Ser Thr
128 65          70          75          80
129 Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Phe Val His Asp
130          85          90          95
131 Leu Thr Asn Lys Lys Ser Ser Gln Asn Leu Arg Arg Trp Ser Leu Glu
132          100          105          110
133 Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val Thr Asn Gly
134          115          120          125
135 Asp Tyr Asp Gln Glu Gln Phe Ala Asp Asn Gln Ile Pro Leu Leu Val
136          130          135          140
137 Ile Gly Thr Lys Leu Asp Gln Ile His Glu Thr Lys Arg His Glu Val
138 145          150          155          160
139 Leu Thr Arg Thr Ala Phe Leu Ala Glu Asp Phe Asn Pro Glu Glu Ile
140          165          170          175
141 Asn Leu Asp Cys Thr Asn Pro Arg Tyr Leu Ala Ala Gly Ser Ser Asn
142          180          185          190
143 Ala Val Lys Leu Ser Arg Phe Phe Asp Lys Val Ile Glu Lys Arg Tyr
144          195          200          205
145 Phe Leu Arg Glu Gly Asn Gln Ile Pro Gly Phe Pro Asp Arg Lys Arg
146          210          215          220
147 Phe Gly Ala Gly Thr Leu Lys Ser Leu His Tyr Asp
148 225          230          235
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 711
152 <212> TYPE: DNA
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 3
156 atggcgctccc tggatcgggt gaaggtactg gtgttgggag actcaggtgt tgggaaatct 60
157 tcgttagtcc atctcctatg ccaaaatcaa gtgctgggaa atccatcatg gactgtgggc 120
158 tgctcagtgg atgtcagagt tcatgattac aaagaaggaa cccagaaga gaagacctac 180
159 tacatagaat tatgggatgt tggaggctct gtgggcagtg ccagcagcgt gaaaagcaca 240
160 agagcagtat tctacaactc cgtaaattgt attattttcg tacacgactt aacaaataag 300
161 aagtcctccc aaaacttgcg tcgttgggtc ttggaagctc tcaacaggga tttggtgcc 360
162 actggagtct tggtgacaaa tggggattat gatcaagaac agtttgctga taaccaaata 420
163 cactgttg taatagggac taaactggac cagattcatg aaacaaagcg ccatgaagtt 480
164 ttaactagga ctgctttcct ggctgaggat ttcaatccag aagaaattaa tttggactgc 540
165 acaaatccac ggtacttagc tgcaggttct tccaatgctg tcaagctcag taggtttttt 600
166 gataaggtca tagagaagag atacttttta agagaaggta atcagattcc aggctttcct 660
167 gatcggaaaa gatttggggc aggaacatta aagagccttc attatgactg a 711
169 <210> SEQ ID NO: 4
170 <211> LENGTH: 191
171 <212> TYPE: PRT
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Consensus amino acid sequence
177 <400> SEQUENCE: 4

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RAW SEQUENCE LISTING

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Input Set: D:\38155-20035.txt

Output Set: N:\CRF3\01302002\I945173.raw

```

178 Gly Leu Gly Phe Leu Lys Ile Phe Leu Lys Leu Leu Gly Leu Trp Asn
179 1 5 10 15
180 Lys Glu Met Arg Ile Leu Ile Leu Gly Leu Asp Asn Ala Gly Lys Thr
181 20 25 30
182 Thr Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro
183 35 40 45
184 Thr Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Lys Phe
185 50 55 60
186 Thr Val Trp Asp Val Gly Gly Gln Glu Ser Leu Arg Pro Leu Trp Arg
187 65 70 75 80
188 Asn Tyr Phe Pro Asn Thr Asp Ala Val Ile Phe Val Val Asp Ser Ala
189 85 90 95
190 Asp Arg Glu Arg Ile Glu Glu Ala Lys Glu Glu Leu His Ala Leu Leu
191 100 105 110
192 Asn Glu Glu Glu Leu Ala Asp Ala Pro Leu Leu Ile Phe Ala Asn Lys
193 115 120 125
194 Gln Asp Leu Pro Gly Ala Met Ser Glu Ala Glu Ile Arg Glu Ala Leu
195 130 135 140
196 Gly Leu His Glu Leu Lys Gly Ser Lys Gly Lys Val Thr Leu Glu Gly
197 145 150 155 160
198 Asp Arg Pro Trp Glu Ile Gln Gly Cys Ser Ala Val Lys Gly Glu Gly
199 165 170 175
200 Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Lys Lys Arg
201 180 185 190
203 <210> SEQ ID NO: 5
204 <211> LENGTH: 198
205 <212> TYPE: PRT
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Consensus amino acid sequence
211 <400> SEQUENCE: 5
212 Lys Leu Val Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu Leu
213 1 5 10 15
214 Ile Arg Phe Thr Asp Asn Lys Phe Val Glu Glu Tyr Ile Pro Thr Ile
215 20 25 30
216 Gly Val Asp Phe Tyr Thr Lys Thr Val Glu Val Asp Gly Lys Thr Val
217 35 40 45
218 Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ala Leu
219 50 55 60
220 Arg Pro Ala Tyr Tyr Arg Gly Ala Gln Gly Phe Leu Leu Val Tyr Asp
221 65 70 75 80
222 Ile Thr Ser Arg Asp Ser Phe Glu Asn Val Lys Lys Trp Leu Glu Glu
223 85 90 95
224 Ile Leu Arg His Ala Asp Lys Asp Glu Asn Val Pro Ile Val Leu Val
225 100 105 110
226 Gly Asn Lys Cys Asp Leu Glu Asp Asp Glu Asp Leu Glu Leu Thr Glu
227 115 120 125
228 Gly Gln Lys Arg Val Val Ser Thr Glu Glu Gly Glu Ala Leu Ala Lys
229 130 135 140

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230 Glu Leu Gly Ala Leu Pro Phe Met Glu Thr Ser Ala Lys Thr Asn Thr
231 145 150 155 160
232 Asn Val Glu Glu Ala Phe Glu Glu Leu Ala Arg Glu Ile Leu Lys Lys
233 165 170 175
234 Val Ser Glu Val Asn Val Asn Leu Asp Gln Pro Ala Lys Lys Lys Lys
235 180 185 190
236 Ser Lys Cys Cys Ile Leu
237 195
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 166
241 <212> TYPE: PRT
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Consensus amino acid sequence
247 <400> SEQUENCE: 6
248 Pro Thr Trp Thr Thr Pro Ser Ser Ser Glu Asp Ser Glu Asn Tyr Pro
249 1 5 10 15
250 Tyr Met Arg Ser Thr Pro Thr Thr Thr Asn Ile Leu Tyr Phe Val Glu
251 20 25 30
252 Phe Tyr Asp Leu Asn Ser Asp Trp Arg Met Cys Arg Gln Gln Arg Glu
253 35 40 45
254 Ser Phe Tyr Lys Asn Ile Asp Gly Ile Val Leu Val Tyr Asn Met Leu
255 50 55 60
256 Glu Leu Ser Ser Gln Asp Ser Leu His Asp Trp Leu Tyr Asp Pro Leu
257 65 70 75 80
258 Arg Gln Ile Cys Lys His Arg His Leu Arg Ile Arg Ser Ile Leu Lys
259 85 90 95
260 Asn His Asn Ala Pro Ile Leu Val Val Gly Thr Asn Leu Asp Lys Leu
261 100 105 110
262 Met Arg Arg Pro Leu Arg Arg Arg Gly Ser Ile Ala His Gln Leu Asn
263 115 120 125
264 Val Glu Glu Met Leu Val Asn Cys Leu Asp Pro Gln Ser Phe Val Asp
265 130 135 140
266 Lys Ser Arg Asn Gln Gly Lys Leu Tyr Gly Phe Leu Asn Arg Val Ile
267 145 150 155 160
268 Glu Phe Lys Glu Gln Phe
269 165
271 <210> SEQ ID NO: 7
272 <211> LENGTH: 50
273 <212> TYPE: PRT
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Consensus amino acid sequence
279 <400> SEQUENCE: 7
280 Val Arg Ile Leu Met Leu Gly Asp Arg Gly Val Gly Lys Thr Ser Leu
281 1 5 10 15
282 Thr Asn Leu Met Ala Thr Thr Glu Ile Thr Pro Thr Pro Asp Ser Arg
283 20 25 30
284 Thr Val Gly Glu Glu Ser Trp His Val Gln Val Arg Leu His Glu Tyr

```

Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/945,173

DATE: 01/30/2002

TIME: 16:21:03

Input Set : D:\38155-20035.txt

Output Set: N:\CRF3\01302002\I945173.raw

L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11